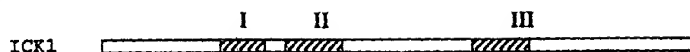


09/733507

A



B

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M V 2

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R K Y R K A G I V E A G V S S T Y M Q 22

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L R S R R I V Y V R S E K S S S V S V V 42

GGTGATAATGGAGTTTCGTCTCTTGTAGTGAAGCAATGAATATAAGAAGAAAGAATTA 240
G D N G V S S S C S G S N E Y K K K E L 62

VI VII
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I H L E E E D K D G D T E T S T Y R R G 82

ACGAAGAGGAAGCTTTTGAATCTGAGAGAGGAGGAGAAAGAAGAAATTAAGTAAATCC 360
T K R K L F E N L R E E E K E E L S K S 102

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M E N Y S S E F E S A V K E S L D C C C 122

AGCGGGAGGAAAACGATGGAGGAGACGGTGACGCGGAGGAGGAGGAGAAGGCCGAAATTG 480
S G R K T M E E T V T A E E E E K A K L 142

ATGACGGAGATGCCAACGGAATCGGAAATTGAAGATTTTTTGTGGAAGCTGAGAAACAA 540
M T E M P T E S E I E D F F V E A E K Q 162

VIII
CTCAAAGAAAATTCAAGAAGAGTACAATTTGATTTGAGAAGGAGAAGCCATTAGAA 600
L K E K F K K K Y N F D F E K E K P L E 182

GGACGTTACGAATGGGTAAAGTTAGAGTGAAGAAGAAGAAGTTTATGGTTTTTTTTT 660
G R Y E W V K L E . 191

TAACTTTTTAGATTTTAATATTTTCAGGAATAAGTTAATTTTATTTTGTGATTGGAAA 720

TATAAGATTGTAGGAGGAATGTTTTTGAAGTACGAAATTGCACAGAAAAGAAGAAAG 780

CTTTTAAACAGATTTTAGAGCCCAGAAAAGTCGTGTCTTTTAGCTCTACTTTTACCTCTT 840

CTTCGAATCTTGTGTATCTTTTAGCATATTCTTTAGTACAATTTTATGTTTTTGGTGA^{*}CT 900

GATA^{*} 905

Characterization of cDNA (Wang et al., 1997) and genomic sequences of *ICK1*.
(A). Genomic organization *ICK1*. Open bars represent exons and filled bars, introns.
(B). Features of cDNA sequence and deduced amino acid sequence.

Figure 1

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SUBSTITUTE SHEET (RULE 26)

008027 205E260

61 ACGTATATGCAGCTACGGAGCCGGAGAAATTGTTTATGTTAGATCGGAAAAATCAAGCTCT Ick1.seq
 3 ACGTATATGCAGCTACGGAGCCGGAGAAATTGTTTATGTTAGATCGGAAAAATCAAGCTCT ICK1b.seq
 6 [REDACTED] GATTTTT [REDACTED] TAG [REDACTED] ICK1c.seq

121 GTCTCCGTCGTCGGTGATAATGGAGTTTCGTCGCTTGTAGTGAAGCAATGAATATAAG Ick1.seq
 63 GTCTCCGTCGTCGGTGATAATGGAG [REDACTED] ICK1b.seq
 18 [REDACTED] ICK1c.seq

181 AAGAAAGAATTAATACATCTGGAGGAGGAAGATAAAGATGGTGACACTGAAACGTCGACG Ick1.seq
 88 [REDACTED] ICK1b.seq
 18 [REDACTED] ICK1c.seq

241 TATCGACGGGGTACGAAGAGGAAGCTTTTTGAAAATCTGAGAGAGGAGGAGAAAGAAGAA Ick1.seq
 88 [REDACTED] ICK1b.seq
 18 [REDACTED] GGGTACGAAGAGGAAGCTTTTTGAAAATCTGAGAGAGGAGGAGAAAGAAGAA ICK1c.seq

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 88 [REDACTED] AATTATTCATCGGAATTTGAATCGGCGGTTAAAGAATCGTTA ICK1b.seq
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361 GATTGTTGTTGTAGCGGGAGGAAAACGATGGAGGAGACGGTGACGGCGGAGGAGGAGGAG Ick1.seq
 130 GATTGTTGTTGTAGCGGGAGGAAAACGATGGAGGAGACGGTGACGGCGGAGGAGGAGGAG ICK1b.seq
 130 GATTGTTGTTGTAGCGGGAGGAAAACGATGGAGGAG [REDACTED] GAGGAG ICK1c.seq

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661 TTGATTTGGAAATATAAGATTGTAGGAGGAATGTTTTAGAAAGTACGAAATTGCACAGA Ick1.seq
 430 TTGATTTGGAAATATA ICK1b.seq
 379 ICK1c.seq

Alignment of *ICK1* cDNA sequence with *ICK1b* and *ICK1c* showing the differences

Figure 2

GTGGAATCTAGGATAAATTCTGTCTCCGTGTGTACAGGCGACGAATCGCGGTGGAATTGTG
GCGAGAATAATCAGCAGAGAGCGTCGGAGACGAGTGTGTTATAGTACGACGCGCAGATTTCT
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GACGATCGTGAAACAGAAACGTCGTGGATTTACGATGATTTGAATAAGAGTGAGGAATCG
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AAGATCTTCGGAATAAGTTGTGGAATGTTCTATGAAGTATAACTTCGATTTCGAGAAA
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TGATGATAATGATGATCATTGTTTTACCAAAGTACTTATTATTTCTCTTCTGTAATAAT
CTTTGCTTTGATTTTTCTTTTAAACAAAATCCAAATGTAGATATCTTCTCTCGAATAATC
AATAACATGTAATCAACTTTTGTTGTACTTCTTGGAGTAATTAATTAGATTCTGTGTT
TTTCTGATTAATAAACTATAAGTTTATAACTAAA

cDNA sequence of *ICK2*

[illegible]

Figure 3

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SUBSTITUTE SHEET (RULE 26)

AAAAAAAAAAGCAGAGAGAGAGAGACACAAAAAATCCAAGAGAGAAAAAATGAGCGAGAGA
 AAGCGAGAGCTTGCAGAAGAAGCTTCAAGCACAAAGCTTCTCACCCTGAAGAAAACGAAG
 CTTAATGATTCTTCTGATTATCACCAGGACTCTCATGACGTCATCGTCTTCGCGGTTTCA
 TCTTCTCCGTTGCTTCGTTCGGCGGGCTTTAGCGTCTGATGAATGTTCCGTTACCATCGGT
 GGAGAAGAAAGTGATCAGTCCTCGAGTATCAGCTCCGGTTGTTTCACCAGTGAATCGAAA
 GAAATCGCGAAGAACAGTTCGTTCGTTTGGTGTAGATCTGGAGGATCATCAAATCGAAACC
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 GAGGGTTTGGGAGAAACGACAACAGAAATGGAATCATCATCGGCAACGAAGAGAAAACAA
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 GAACCGCTTGAAGGTCGCTACAAGTGGGATCGACTTTAAGCCATCAAAAAGCAAATACCA
 TCCATGAAGAAGACAAAAGAAAAATAGGTTTTGTTTTTCGTGGTTAACATTTCCACTTGT
 ACAGCTCTAGTCTATTTCTCTTTAAAAACCTATGTTACTAGTTCGTACAAAACAAAACAA
 AAAACACGACCTTTATAATGAAATTTCCGATCTTGGCTACTAAA

cDNA sequence of *ICN2*

Figure 4

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SUBSTITUTE SHEET (RULE 26)

003021 2055E/60

[illegible]

cDNA sequence of ICN6

[illegible]

Figure 5

ATTAAAGAGTCTGGTTCAGGCTCTCGCGTTGACTCGGTTAACTCGGCTCCTGTAGCTCAG
AGCTCTAATGAAGATGAATGTTTTGACAATTTCTGTAGTGTCCAAGTTTCTTGTGGTGAA
AACAGTCTCGGTTTTGAATCAAGACACAGGCACAAGGAGGACGACGCCTTGTAACTTTGTT
GAGGATATGGAGATCATGTTTACACCAGGGTCTAGCAGAGGTCGATGTGCAGAGCAACC
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TTTGCATATGCAGAGCAGCAGCAACAGAGGCTATTATGGAGAAGTACAACCTCGACATT
GTGAATGATATCCCCCTCGCGGACGTTACGAATGGGTGCAAGTCAAACTGATGAAGTTCA
AAAGGAAACAGCTCCAAAGACATGGTGTGAAGTTAGAGAATTGTGATGGAGTTTAACAG
AACTAAACCAACATCAGAAATCGTGTAACTCTTAAGTTAATAATGTGGGTTA

cDNA sequence of ICN7

SEQ ID NO. 15: The nucleotide sequence of *Chenopodium rubrum* CDK11 (GenBank AJ002173)

gcacgagcgaaattcggttgtaggaggttaaaccagagctcgagactgccctagctatggcggcagctgctactccaac
ttcgtctccggcgagaagatcaagaaggttcgaagtcgtctataattcctaactaagaagtcgtcgaagaatt
tgicggcgccggagaatttcgccgaattgaaacgacgccgttggaagtgcggcggttgtaggagggaagaggttgcg
aattgtctcgagtagcgaggttaattactacagctaggtcggattttccgccgtctgttgcctcaagcaattatgatcgtt
gagttctagcgcgagccagaagttagttaaggatgatgatgtttgggaaatctacagcagatccagaggttgagagtggtg
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gaaattgcgaagttaattcttaatttagccctttctttcttttagcagaagtgatctattctcacaccgaaaaaaaa
aaaa

SEQ ID NO. 16: The amino acid sequence of *Chenopodium rubrum* CDK1
 MAAAATPTSS PAKKIKKVS K SSYNPQLRS RRKNLSAPEN FAELETTPL
 VAAVVEEEEVANCCSSSEVT TARSDFPPSC CSSNYDQLSS SEPEVVKDDD
 GLGNRTADPE VESGEASKT KESHRTEARE ATKLDDQDYP ATKSTVQIKM
 PSDSEIEEFF AVAEKDLOKR FSEKYNFIDV KDVP LKGRYD WVPINP

Figure 6

```

Consensus 'Consensus #1': When 60% (3) match the residue of the Consensus show the residue of the
Consensus, otherwise show '.'.

Decoration 'Decoration #1': Shade (with black at 40% fill) residues that match the consensus named
'Consensus #1' exactly.

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Alignment of deduced amino acid sequences of ICK1, ICK2, ICN2, ICN6 and ICN7

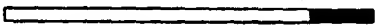
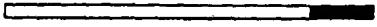
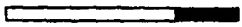
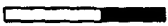

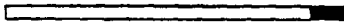
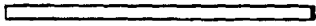
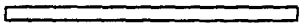
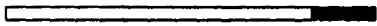
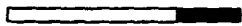
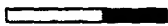




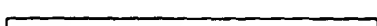
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cdc2a	/		0.0
/	(3-191)		0.0
cdc2a	(3-191)		12.4
cdc2a	(73-191)		40.6
cdc2a	(109-191)		42.6
cdc2a	(154-191)		10.7
cdc2a	(3-175)		0.3
cdc2a	(3-162)		0.3
cdc2a	(3-152)		0.0
cyclin δ3	/		0.8
cyclin δ3	(3-191)		100.0
cyclin δ3	(73-191)		397.3
cyclin δ3	(109-191)		480.7
cyclin δ3	(154-191)		7.1
cyclin δ3	(3-175)		19.9
cyclin δ3	(3-162)		2.5
cyclin δ3	(3-152)		2.2
ATMPK2	(3-191)		0.0

Figure 8